

Per/09 JK

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 8/22/2001  
Edited by:                       
Verified by:                      (STIC staff)

Serial Number: 09/744,176

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☒ Deleted extra, invalid, headings used by an applicant, specifically:                     C1107
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

## RAW SEQUENCE LISTING

DATE: 08/22/2001

PATENT APPLICATION: US/09/744,176

TIME: 16:11:45

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\08222001\I744176.raw

3 <110> APPLICANT: Connex - Gesellschaft zur Optimierung von Forschung und Entwicklung  
 mbH  
 4 INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (I.N.S.E.R.M.)  
 6 <120> TITLE OF INVENTION: Anti Hepatitis C virus antibody and uses thereof  
 8 <130> FILE REFERENCE: B3070PCT  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/744,176  
 C--> 10 <141> CURRENT FILING DATE: 2001-06-18  
 10 <150> PRIOR APPLICATION NUMBER: EP 98 11 35 95.7  
 11 <151> PRIOR FILING DATE: 1998-07-21  
 13 <160> NUMBER OF SEQ ID NOS: 6  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 324  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Homo sapiens  
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 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: (1)..(324)  
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 28 Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln  
 29 1 5 10 15  
 31 acg gcc agg atc acc tgc tct gga gat gca ttg cca aag caa tat gct 96  
 32 Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Gln Tyr Ala  
 33 20 25 30  
 35 tac tgg tat cag cag aag cca ggc cag gcc cct gtg ttg gtg ata tat 144  
 36 Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr  
 37 35 40 45  
 39 aaa gat aat gag agg ccc tca ggg atc cct gag cga ttc tct ggc tcc 192  
 40 Lys Asp Asn Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser  
 41 50 55 60  
 43 agg tca ggg aca aca gtc acg ttg acc atc agt gga gtc cag gca gaa 240  
 44 Arg Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu  
 45 65 70 75 80  
 47 gac gag gct gac tat tac tgt caa tca gca gac agc agt ggt tct tcc 288  
 48 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ala Asp Ser Ser Gly Ser Ser  
 49 85 90 95  
 51 tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta 324  
 52 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
 53 100 105  
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 58 <212> TYPE: PRT  
 59 <213> ORGANISM: Homo sapiens  
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 62 Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln  
 63 1 5 10 15  
 65 Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Gln Tyr Ala

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68 Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
69          35          40          45
71 Lys Asp Asn Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
72          50          55          60
74 Arg Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
75 65          70          75          80
77 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ala Asp Ser Ser Gly Ser Ser
78          85          90          95
80 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
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86 <211> LENGTH: 351
87 <212> TYPE: DNA
88 <213> ORGANISM: Homo sapiens
90 <220> FEATURE:
91 <221> NAME/KEY: CDS
92 <222> LOCATION: (1)..(351)
94 <400> SEQUENCE: 3
95 cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag cct tcg gag 48
96 Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
97 1          5          10          15
99 acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tcc tta agt ggt tac 96
100 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Leu Ser Gly Tyr
101          20          25          30
103 ttc tgg acc tgg atc cgc cag tcc ccc ggg aag ggg ctg gag tgg att 144
104 Phe Trp Thr Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
105          35          40          45
107 ggg gaa agc aat tat agt gga agt acc agg tac aac ccg tcc ctc aag 192
108 Gly Glu Ser Asn Tyr Ser Gly Ser Thr Arg Tyr Asn Pro Ser Leu Lys
109          50          55          60
111 agt cga gtc acc ata tca gta gac acg tcc cag aac cag ttc tcc ctg 240
112 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Gln Asn Gln Phe Ser Leu
113 65          70          75          80
115 aag ctg agc tct gtg acc gcc gcg gac acg gct gta tat tac tgt gcg 288
116 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
117          85          90          95
119 aga ggt tgg gcg gtg gac ggt atg gac gtc tgg ggc caa ggg acc acg 336
120 Arg Gly Trp Ala Val Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr
121          100          105          110
123 gtc acc gtc tcc tca 351
124 Val Thr Val Ser Ser
125          115
128 <210> SEQ ID NO: 4
129 <211> LENGTH: 117
130 <212> TYPE: PRT
131 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 4
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135      1              5              10              15
137 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Leu Ser Gly Tyr
138              20              25              30
140 Phe Trp Thr Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
141              35              40              45
143 Gly Glu Ser Asn Tyr Ser Gly Ser Thr Arg Tyr Asn Pro Ser Leu Lys
144              50              55              60
146 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Gln Asn Gln Phe Ser Leu
147 65              70              75              80
149 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
150              85              90              95
152 Arg Gly Trp Ala Val Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr
153              100              105              110
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162 <212> TYPE: DNA
163 <213> ORGANISM: Homo sapiens
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166 <221> NAME/KEY: CDS
167 <222> LOCATION: (1)..(324)
169 <400> SEQUENCE: 5
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171 Ser Ser Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
172 1              5              10              15
174 acg gcc agg atc acc tgc tct gga gat gca ttg cca aag caa tat gct 96
175 Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Gln Tyr Ala
176              20              25              30
178 tac tgg tat cag cag aag cca ggc cag gcc cct gtg ttg gtg ata tat 144
179 Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
180              35              40              45
182 aaa gat aat gag agg ccc tca ggg atc cct gag cga ttc tct ggc tcc 192
183 Lys Asp Asn Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
184              50              55              60
186 agg tca ggg aca aca gtc acg ttg acc atc agt gga gtc cag gca gaa 240
187 Arg Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
188 65              70              75              80
190 gac gag gct gac tat tac tgt caa tca gca gac agc agt ggt tct tcc 288
191 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ala Asp Ser Ser Gly Ser Ser
192              85              90              95
194 tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta 324
195 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
196              100              105
199 <210> SEQ ID NO: 6
200 <211> LENGTH: 108
201 <212> TYPE: PRT
202 <213> ORGANISM: Homo sapiens
204 <400> SEQUENCE: 6

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205 Ser Ser Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
206   1           5           10           15
208 Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Gln Tyr Ala
209           20           25           30
211 Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
212           35           40           45
214 Lys Asp Asn Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
215           50           55           60
217 Arg Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
218   65           70           75           80
220 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ala Asp Ser Ser Gly Ser Ser
221           85           90           95
223 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
224           100          105

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/744,176

DATE: 08/22/2001

TIME: 16:11:46

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\08222001\I744176.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date